



PubMed	Nucleotide	Protein	Genome	Structure	PopSet	Taxonomy	OMIM	
Search PubMed	<input checked="" type="checkbox"/> for						Go	Clear
		Limits	Preview/Index	History	Clipboard			
Display	Abstract	<input checked="" type="checkbox"/>	Save	Text	Order	Add to Clipboard		

Entrez PubMed

☐ 1: Mol Cell Biol 1987 Oct;7(10):3818-21

Related Articles, Books

PubMed Services

Regulation by the yeast mating-type locus of STE12, a gene required for cell-type-specific expression.

Fields S, Herskowitz I.

Department of Microbiology, State University of New York at Stony Brook 11794.

Related Resources

The STE12 gene of the yeast *Saccharomyces cerevisiae* is necessary for RNA synthesis from two sets of cell-type-specific genes. We isolated a recombinant plasmid that carries the STE12 gene by complementation of the mating defect of *ste12* cells. The DNA of the cloned gene was used to disrupt the chromosomal STE12 gene and to identify the STE12 transcript. We show that the STE12 transcript level is repressed 5- to 10-fold in *a/alpha* cells. The STE12 product thus acts to promote diploidy by activating expression of the two sets of genes necessary for mating, and then its synthesis is repressed by products unique to the diploid cell type.

PMID: 2824997 [PubMed - indexed for MEDLINE]

Display	Abstract	<input checked="" type="checkbox"/>	Save	Text	Order	Add to Clipboard
---------	----------	-------------------------------------	------	------	-------	------------------

Write to the Help Desk
NCBI | NLM | NIH
Department of Health & Human Services
Freedom of Information Act | Disclaimer

500 12

Signal seq's -
don't need yet

RESULT 1
LZCH
lysozyme (EC 3.2.1.17) c precursor [validated] - chicken
N;Alternate names: 1,4-beta-N-acetylmuramidase c; peptidoglycan N-acetylmuramoylhydrolase c
C;Species: Gallus gallus (chicken)
C;Date: 31-May-1979 #sequence_revision 31-May-1979 #text_change 15-Sep-2000
C;Accession: A93859; B93859; A41423; A92209; A92017; S23310; S65910; A00853; S51218
R;Jung, A.; Sippel, A.E.; Grez, M.; Schutz, G.
Proc. Natl. Acad. Sci. U.S.A. 77, 5759-5763, 1980
A;Title: Exons encode functional and structural units of chicken lysozyme.
A;Reference number: A93859; MUID:81077254
A;Accession: A93859
A;Molecule type: DNA
A;Residues: 1-147 <JU1>
A;Cross-references: GB:J00885; NID:g212274; PIDN:AAA48943.1; PID:g212276
A;Accession: B93859
A;Molecule type: mRNA
A;Residues: 1-48,'V',50-123,'S',125-147 <JU2>
A;Cross-references: GB:V00428; NID:g63580; PIDN:CAA23711.1; PID:g63581
A;Note: these differences may have arisen during construction of the cDNA plasmid
R;Kumagai, I.; Kojima, S.; Tamaki, E.; Miura, K.
J. Biochem. 102, 733-740, 1987
A;Title: Conversion of trp 62 of hen egg-white lysozyme to tyr by site-directed mutagenesis.
A;Reference number: A41423; MUID:88139224
A;Accession: A41423
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-147 <KUM>
A;Experimental source: hen oviduct
A;Note: a site-directed mutant with Trp-80 replaced by Tyr showed enhanced bacteriolytic activity
R;Palmiter, R.D.; Gagnon, J.; Ericsson, L.H.; Walsh, K.A.
J. Biol. Chem. 252, 6386-6393, 1977
A;Title: Precursor of egg white lysozyme. Amino acid sequence of an NH-2-terminal extension.
A;Reference number: A92209; MUID:77249586
A;Accession: A92209
A;Molecule type: protein
A;Residues: 1-20 <PAL>
R;Canfield, R.
J. Biol. Chem. 238, 2698-2707, 1963
A;Title: The amino acid sequence of egg white lysozyme.
A;Reference number: A92017
A;Accession: A92017
A;Molecule type: protein
A;Residues: 19-120,'D',122-147 <CAN>
R;Tsugita, A.; Takamoto, K.; Kamo, M.; Iwadate, H.
Eur. J. Biochem. 206, 691-696, 1992
A;Title: C-terminal sequencing of protein. A novel partial acid hydrolysis and analysis by mass spectrometry.
A;Reference number: S23188; MUID:92298996
A;Accession: S23310
A;Molecule type: protein

A;Residues: 19-45;121-147 <TSU>
 R;Canfield, R.; Liu, A.K.
 J. Biol. Chem. 240, 1997-2002, 1965
 A;Title: The disulfide bonds of egg white lysozyme (muramidase).
 A;Reference number: A92019
 A;Contents: annotation; disulfide bonds
 R;Jauregui-Adell, J.; Jolles, J.; Jolles, P.
 Biochim. Biophys. Acta 107, 97-111, 1965
 A;Title: The disulfide bridges of hen's egg-white lysozyme.
 A;Reference number: A90570; MUID:66076966
 A;Contents: annotation; disulfide bonds
 R;Imoto, T.; Johnson, L.N.; North, A.C.T.; Phillips, D.C.; Rupley, J.A.
 in The Enzymes, 3rd ed., vol.7, Boyer, P.D., ed., pp.665-868, Academic Press,
 New York and London, 1972
 A;Title: Vertebrate lysozymes.
 A;Reference number: A94444
 A;Contents: annotation; X-ray crystallography, 2.0 angstroms; review
 R;Diamond, R.; Phillips, D.C.; Blake, C.C.F.; North, A.C.T.
 submitted to the Brookhaven Protein Data Bank, February 1975
 A;Reference number: A50763; PDB:6LYZ
 A;Contents: annotation; X-ray crystallography, 1.8 angstroms, residues 19-147
 R;Diamond, R.
 J. Mol. Biol. 82, 371-391, 1974
 A;Title: Real-space refinement of the structure of hen egg-white lysozyme.
 A;Reference number: A58453; MUID:74127120
 A;Contents: annotation; X-ray crystallography, 2.0 angstroms
 R;Hodsdon, J.M.; Brown, G.M.; Sieker, L.C.; Jensen, L.H.
 submitted to the Brookhaven Protein Data Bank, April 1985
 A;Reference number: A50266; PDB:1LZT
 A;Contents: annotation; X-ray crystallography, triclinic habit, 1.97
 angstroms, residues 19-147
 R;Kurachi, K.; Sieker, L.C.; Jensen, L.H.
 J. Mol. Biol. 101, 11-24, 1976
 A;Title: Structures of triclinic mono- and di-N-acetylglucosamine: lysozyme
 complexes - a crystallographic study.
 A;Reference number: A58454; MUID:76146540
 A;Contents: annotation; X-ray crystallography, triclinic habit, 1.97
 angstroms, residues 19-147
 R;Kodandapani, R.; Suresh, C.G.; Vijayan, M.
 submitted to the Brookhaven Protein Data Bank, July 1990
 A;Reference number: A50949; PDB:4LYM
 A;Contents: annotation; X-ray crystallography, 2.1 angstroms, residues 19-147
 R;Kodandapani, R.; Suresh, C.G.; Vijayan, M.
 J. Biol. Chem. 265, 16126-16131, 1990
 A;Title: Crystal structure of low humidity tetragonal lysozyme at 2.1-
 angstrom resolution. Variability in hydration shell and its structural
 consequences.
 A;Reference number: A37878; MUID:90375467
 A;Contents: annotation; X-ray crystallography, 2.1 angstroms, residues 19-147
 R;Smith, L.J.; Sutcliffe, M.J.; Redfield, C.; Dobson, C.M.
 submitted to the Brookhaven Protein Data Bank, August 1992
 A;Reference number: A51239; PDB:1HWA
 A;Contents: annotation; conformation by (1)H-NMR, residues 19-147
 R;Smith, L.J.; Sutcliffe, M.J.; Redfield, C.; Dobson, C.M.
 J. Mol. Biol. 229, 930-944, 1993
 A;Title: Structure of hen lysozyme in solution.
 A;Reference number: A58443; MUID:93188024

A;Contents: annotation; conformation by (1)H-NMR, residues 19-147
 R;Redfield, C.; Dobson, C.M.
 Biochemistry 27, 122-136, 1988
 A;Title: Sequential (1)H NMR assignments and secondary structure of hen egg white lysozyme in solution.
 A;Reference number: A30625; MUID:88163558
 A;Contents: annotation; conformation by (1)H-NMR, residues 19-147
 R;Fukamizo, T.; Hatta, T.; Goto, S.
 Eur. J. Biochem. 231, 56-64, 1995
 A;Title: Hen-egg-white lysozyme modified with histamine. State of the imidazolylethyl group covalently attached to the binding site and its effect on the sugar-binding ability.
 A;Reference number: S65910; MUID:95354703
 A;Accession: S65910
 A;Molecule type: protein
 A;Residues: 116-118,'X',120-130 <FUK>
 C;Comment: Lysozyme c has been found in the egg white and polymorphonuclear leukocytes.
 C;Comment: Lysozymes are primarily bacteriolytic; those in tissues and body fluids are associated with the monocyte-macrophage system and enhance the activity of immunoagents.
 C;Genetics:
 A;Introns: 46/1; 100/1; 126/1
 C;Function:
 A;Description: catalyzes hydrolysis of the beta-1,4-glycosidic bond between N-acetylmuramic acid and N-acetylglucosamine in peptidoglycan and other complex polysaccharides
 A;Note: this protein has hydrolytic and transglycosylation activities, and slight esterase activity; it acts rapidly on both peptide-substituted and unsubstituted peptidoglycan and, slowly, on chitin oligosaccharides
 C;Superfamily: lysozyme c
 C;Keywords: bacteriolytic enzyme; egg white; glycosidase; hydrolase; leukocyte; polysaccharide degradation
 F;1-18/Domain: signal sequence #status experimental <SIG>
 F;19-147/Product: lysozyme c #status experimental <MAT>
 F;24-145,48-133,82-98,94-112/Disulfide bonds: #status experimental
 F;53,70/Active site: Glu, Asp #status experimental
 F;119/Binding site: substrate (Asp) #status experimental

Query Match 100.0%; Score 86; DB 1; Length 147;
 Best Local Similarity 100.0%; Pred. No. 1.9e-05;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 mrsllilvlcflplaalg 18
 |||||
 Db 1 MRSLLILVLCFLPLAALG 18

S&G 3

RESULT 1

JFBY1

mating pheromone alpha-1 precursor - yeast (*Saccharomyces cerevisiae*)

N;Alternate names: mating factor alpha; mating hormone alpha-1; protein P2209; protein YPL187w

C;Species: *Saccharomyces cerevisiae*

C;Date: 24-Apr-1984 #sequence_revision 26-Jul-1996 #text_change 16-Jun-2000

C;Accession: S65199; S65206; A01413; S05790; A91241; A91943

R;Benes, V.; Rechmann, S.; Nentwich, U.; Voss, H.; Ansorge, W.
submitted to the Protein Sequence Database, May 1996

A;Reference number: S65183

A;Accession: S65199

A;Molecule type: DNA

A;Residues: 1-165 <BEN>

A;Cross-references: EMBL:Z73543; NID:g1370390; PIDN:CAA97899.1; PID:g1370391; GSPDB:GN00016; MIPS:YPL187w

A;Experimental source: strain S288C (AB972)

R;Rieger, M.; Mueller-Auer, S.; Schaefer, M.
submitted to the Protein Sequence Database, May 1996

A;Reference number: S65202

A;Accession: S65206

A;Molecule type: DNA

A;Residues: 1-165 <RIE>

A;Cross-references: EMBL:Z73543; NID:g1370390; PIDN:CAA97899.1; PID:g1370391; GSPDB:GN00016; MIPS:YPL187w

A;Experimental source: strain S288C (AB972)

R;Kurjan, J.; Herskowitz, I.
Cell 30, 933-943, 1982

A;Title: Structure of a yeast pheromone gene (MFalpha): a putative alpha-factor precursor contains four tandem copies of mature alpha-factor.

A;Reference number: A90827; MUID:83050979

A;Accession: A01413

A;Molecule type: DNA

A;Residues: 1-41,'S',43-165 <KUR>

A;Cross-references: EMBL:J01340; NID:g171941; PIDN:AAA88727.1; PID:g1197054

A;Experimental source: strain AB320

R;Singh, A.; Chen, E.Y.; Lugovoy, J.M.; Chang, C.N.; Hitzeman, R.A.; Seeburg, P.H.
Nucleic Acids Res. 11, 4049-4063, 1983

A;Title: *Saccharomyces cerevisiae* contains two discrete genes coding for the alpha-factor pheromone.

A;Reference number: S05790; MUID:83246532

A;Accession: S05790

A;Molecule type: DNA

A;Residues: 1-165 <SIN>

A;Cross-references: EMBL:X01581; NID:g3938; PIDN:CAA25734.1; PID:g3939

R;Stoetzler, D.; Kiltz, H.H.; Duntze, W.
Eur. J. Biochem. 69, 397-400, 1976

A;Title: Primary structure of alpha-factor peptides from *Saccharomyces cerevisiae*.

A;Reference number: A91241

A;Accession: A91241

A;Molecule type: protein

A;Residues: 90-102 <STO>

A;Experimental source: strain X2180-1B

R;Tanaka, T.; Kita, H.; Murakami, T.; Narita, K.
J. Biochem. 82, 1681-1687, 1977

A;Title: Purification and amino acid sequence of mating factor from
Saccharomyces cerevisiae.
 A;Reference number: A91943; MUID:78087498
 A;Accession: A91943
 A;Molecule type: protein
 A;Residues: 90-102 <TAN>
 A;Experimental source: strain X2180-1B
 C;Genetics:
 A;Gene: SGD:MF(ALPHA)1; MFA1; MIPS:YPL187w
 A;Cross-references: SGD:S0006108; MIPS:YPL187w
 A;Map position: 16L
 C;Function:
 A;Description: mediates the conjugation process between the two mating types
 by inhibiting the initiation of DNA synthesis in type A cells and
 synchronizing them with type alpha
 C;Superfamily: mating hormone alpha precursor
 C;Keywords: duplication; extracellular protein; glycoprotein; hormone; tandem
 repeat
 F;1-19/Domain: signal sequence #status predicted <SIG>
 F;84-102,103-123,124-144,145-165/Region: 21-residue repeats
 F;90-102/Product: mating pheromone alpha #status experimental <MAT1>
 F;111-123/Product: mating pheromone alpha #status experimental <MAT2>
 F;132-144/Product: mating pheromone alpha #status experimental <MAT3>
 F;153-165/Product: mating pheromone alpha #status experimental <MAT4>
 F;23,57,67/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 88; DB 1; Length 165;
 Best Local Similarity 100.0%; Pred. No. 2.5e-07;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps
 0;

```

Qy      1 mrfpsiftavlfaassala 19
          |||||
Db      1 MRFPSIFTAVLFAASSALA 19
  
```